

SEQUENCE LISTING

<110> Kimura, Naoki
Tsuchiya, Masayuki
Nanami, Masahiko
Tomimatsu, Takashi
Kawai, Shigeto

<120> Cell Death Inducing Agents

<130> 14875-166US1

<150> PCT/JP2004/018501

<151> 2004-12-10

<150> JP 2003-415758

<151> 2003-12-12

<160> 20

<170> PatentIn version 3.1

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<212> DNA

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<222> (14)..(1561)

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Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser	
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ggc tac acc ttc aca gac tac ttt ata cac tgg gtg aaa cag agg cct	193
Gly Tyr Thr Phe Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro	
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Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr	
65 70 75	
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Thr Asp Tyr Asn Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp	
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Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro	
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Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys	
225 230 235	
cag caa agg acg agt tat cca ccc acg ttc ggc tgc ggg aca aag ttg	769
Gln Gln Arg Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu	
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Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly	
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Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro	
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Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr	
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Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu	
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gcc	tac	att	ttg	ctc	agc	agc	ctg	acc	tct	gag	gac	tct	gcg	atg	tat		1105
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Phe	Cys	Val	Arg	Ser	Asp	Asp	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr		
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Leu	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly		
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Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser		
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Val	Ser	Tyr	Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Phe	Pro	Lys		
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Leu	Trp	Ile	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Thr	Arg		
445					450				455						460		
ttc	agt	ggc	agt	gga	tct	ggg	acc	tct	tac	tct	ctc	aca	atc	agc	cga		1441
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg		
				465				470						475			
atg	gag	gct	gaa	gat	gct	gcc	act	tat	tac	tgc	cag	caa	agg	acg	agt		1489
Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Thr	Ser		
			480				485						490				
tat	cca	ccc	acg	ttc	ggc	tcg	ggg	aca	aag	ttg	gag	ata	aaa	gac	tac		1537
Tyr	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Asp	Tyr		
		495					500					505					
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Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	35	40	45	
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Glu	Lys	Phe	Arg	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	85	90	95	
Thr	Ala	Tyr	Ile	Leu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Met	100	105	110	
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Gly	Gly	Gly	Gly	Ser	Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	145	150	155	160
Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	165	170	175	
Ser	Val	Ser	Tyr	Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Phe	Pro	180	185	190	
Lys	Leu	Trp	Ile	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Thr	195	200	205	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	210	215	220	
Arg	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Arg	Thr	225	230	235	240
Ser	Tyr	Pro	Pro	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	245	250	255	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	260	265	270	
Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	Val	275	280	285	
Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Phe	Ile	290	295	300	

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp
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 Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg Gly
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 Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Ile Leu
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 Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met Tyr Phe Cys Val Arg
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 Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 370 375 380
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 385 390 395 400
 Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 405 410 415
 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 420 425 430
 His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys Leu Trp Ile Tyr
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 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg Phe Ser Gly Ser
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 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
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1				5					10					15		

gtc	cat	tgc	cag	gtc	cag	ttg	cag	cag	tct	gga	cct	gag	ctg	gtg	aag	96
Val	His	Cys	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	
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cct	ggg	gct	tca	gtg	aag	atg	tct	tgt	aag	gct	tct	ggc	tac	acc	ttc	144
Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
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Glu	Trp	Ile	Gly	Trp	Ile	Phe	Pro	Gly	Asp	Asp	Thr	Thr	Asp	Tyr	Asn	
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gag	aag	ttc	agg	ggc	aag	acc	aca	ctg	act	gca	gac	aaa	tcc	tcc	agc	288
Glu	Lys	Phe	Arg	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	
			85						90					95		

aca	gcc	tac	att	ttg	ctc	agc	agc	ctg	acc	tct	gag	gac	tct	gcg	atg	336
Thr	Ala	Tyr	Ile	Leu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Met	
			100					105					110			

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Tyr	Phe	Cys	Val	Arg	Ser	Asp	Asp	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	
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			20					25					30			

Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35						40				45				

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 Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn
 65 70 75 80
 Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met
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 Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
 20 25 30
 atg tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc 144
 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
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 tca agt gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt 192
 Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe
 50 55 60
 ccc aaa ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct 240
 Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 act cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc 288
 Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 agc cga atg gag gct gaa gat gct gcc act tat tac tgc cag caa agg 336
 Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg
 100 105 110

acg agt tat cca ccc acg ttc ggc tcg ggg aca aag ttg gag ata aaa 384
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 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe
 50 55 60
 Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
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 gtc cat tgc cag gtc cag ttg cag cag tct gga cct gag ctg gtg aag 96
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Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
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Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn
 65 70 75 80

Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met
 100 105 110

Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
 115 120 125

Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met
 145 150 155 160

Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser
 165 170 175

Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro
 180 185 190

Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr
 195 200 205

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
 210 215 220

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr
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Tyr Lys Asp Asp Asp Asp Lys

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SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Cell Death Inducing Agent

<130> C1-A0323P

<150> JP 2003-415758

<151> 2003-12-12

<160> 20

<170> PatentIn version 3.1

<210> 1

<211> 1572

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (14)..(1561)

<223>

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Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser

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10

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Ile Thr Ala Gly Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro

15

20

25

gag ctg gtg aag cct ggg gct tca gtg aag atg tct tgt aag gct tct 145

Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser

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Gly Tyr Thr Phe Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro			
45	50	55	60
gga cag gga ctt gaa tgg att gga tgg att ttt cct gga gat gat act			241
Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr			
	65	70	75
act gat tac aat gag aag ttc agg ggc aag acc aca ctg act gca gac			289
Thr Asp Tyr Asn Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp			
	80	85	90
aaa tcc tcc agc aca gcc tac att ttg ctc agc agc ctg acc tct gag			337
Lys Ser Ser Ser Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu			
	95	100	105
gac tct gcg atg tat ttc tgt gta agg agt gac gac ttt gac tac tgg			385
Asp Ser Ala Met Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp			
	110	115	120
ggc cag ggc acc act ctc aca gtc tcc tca ggt gga ggc ggt tca ggc			433
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly			
	125	130	135
gga ggt ggc tct ggc ggt ggc gga agc caa att gtt ctc acc cag tcg			481
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser			
	145	150	155
cca gca atc atg tct gca tct cca ggg gag aag gtc acc ata acc tgc			529
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys			
	160	165	170
agt gcc agc tca agt gta agt tac atg cac tgg ttc cag cag aag cca			577
Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro			

175	180	185	
ggc act ttt ccc aaa ctc tgg att tat agc aca tcc aac ctg gct tct			625
Gly Thr Phe Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser			
190	195	200	
gga gtc cct act cgc ttc agt ggc agt gga tct ggg acc tct tac tct			673
Gly Val Pro Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser			
205	210	215	220
ctc aca atc agc cga atg gag gct gaa gat gct gcc act tat tac tgc			721
Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys			
	225	230	235
cag caa agg acg agt tat cca ccc acg ttc ggc tcg ggg aca aag ttg			769
Gln Gln Arg Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu			
	240	245	250
gag ata aaa gga ggt ggt ggc agt ggt ggc ggc gga tcc ggt ggc ggt			817
Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly			
	255	260	265
ggc tca cag gtc cag ttg cag cag tct gga cct gag ctg gtg aag cct			865
Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro			
	270	275	280
ggg gct tca gtg aag atg tct tgt aag gct tct ggc tac acc ttc aca			913
Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr			
	285	290	295
gac tac ttt ata cac tgg gtg aaa cag agg cct gga cag gga ctt gaa			961
Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu			
	305	310	315
tgg att gga tgg att ttt cct gga gat gat act act gat tac aat gag			1009
Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu			

320	325	330	
aag ttc agg ggc aag acc aca ctg act gca gac aaa tcc tcc agc aca			1057
Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr			
335	340	345	
gcc tac att ttg ctc agc agc ctg acc tct gag gac tct gcg atg tat			1105
Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met Tyr			
350	355	360	
ttc tgt gta agg agt gac gac ttt gac tac tgg ggc cag ggc acc act			1153
Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr			
365	370	375	380
ctc aca gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc			1201
Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly			
385	390	395	
ggt ggc gga agc caa att gtt ctc acc cag tcg cca gca atc atg tct			1249
Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser			
400	405	410	
gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt			1297
Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser			
415	420	425	
gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt ccc aaa			1345
Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys			
430	435	440	
ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct act cgc			1393
Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg			
445	450	455	460
ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga			1441
Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg			

	465	470	475	
atg gag gct gaa gat gct gcc act tat tac tgc cag caa agg acg agt				1489
Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser				
	480	485	490	
tat cca ccc acg ttc ggc tgc ggg aca aag ttg gag ata aaa gac tac				1537
Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr				
	495	500	505	
aag gat gac gac gat aag tga taa gcggccgcaa t				1572
Lys Asp Asp Asp Asp Lys				
510				

<210> 2
 <211> 514
 <212> PRT
 <213> Mus musculus

<400> 2	
Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly	
1	15
Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys	
20	30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35	45
Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu	
50	60
Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn	
65	80

Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met
100 105 110

Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125

Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met
145 150 155 160

Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser
165 170 175

Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro
180 185 190

Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr
195 200 205

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
210 215 220

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr
225 230 235 240

Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Gly
245 250 255

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
260 265 270

Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val
 275 280 285

Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Phe Ile
 290 295 300

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp
 305 310 315 320

Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg Gly
 325 330 335

Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Ile Leu
 340 345 350

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met Tyr Phe Cys Val Arg
 355 360 365

Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 370 375 380

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 385 390 395 400

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 405 410 415

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 420 425 430

His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys Leu Trp Ile Tyr
 435 440 445

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg Phe Ser Gly Ser
 450 455 460

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
 465 470 475 480

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser Tyr Pro Pro Thr
 485 490 495

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp
 500 505 510

Asp Lys

<210> 3
 <211> 5
 <212> PRT
 <213> Mus musculus

<400> 3
 Asp Tyr Phe Ile His
 1 5

<210> 4
 <211> 17
 <212> PRT
 <213> Mus musculus

<400> 4
 Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg
 1 5 10 15

Gly

<210> 5
<211> 6
<212> PRT
<213> Mus musculus

<400> 5
Ser Asp Asp Phe Asp Tyr
1 5

<210> 6
<211> 10
<212> PRT
<213> Mus musculus

<400> 6
Ser Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 7
<211> 7
<212> PRT
<213> Mus musculus

<400> 7
Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 8
<211> 9
<212> PRT
<213> Mus musculus

<400> 8

Gln Gln Arg Thr Ser Tyr Pro Pro Thr

1

5

<210> 9

<211> 402

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(402)

<223>

<400> 9

atg cga tgg agc tgg atc ttt ctc ttc ctc ctg tca ata act gca ggt 48

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly

1

5

10

15

gtc cat tgc cag gtc cag ttg cag cag tct gga cct gag ctg gtg aag 96

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys

20

25

30

cct ggg gct tca gtg aag atg tct tgt aag gct tct ggc tac acc ttc 144

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35

40

45

aca gac tac ttt ata cac tgg gtg aaa cag agg cct gga cag gga ctt 192

Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu

50

55

60

gaa tgg att gga tgg att ttt cct gga gat gat act act gat tac aat 240

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn

65

70

75

80

gag aag ttc agg ggc aag acc aca ctg act gca gac aaa tcc tcc agc 288
 Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser

85

90

95

aca gcc tac att ttg ctc agc agc ctg acc tct gag gac tct gcg atg 336
 Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met

100

105

110

tat ttc tgt gta agg agt gac gac ttt gac tac tgg ggc cag ggc acc 384
 Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr

115

120

125

act ctc aca gtc tcc tca 402
 Thr Leu Thr Val Ser Ser

130

<210> 10

<211> 134

<212> PRT

<213> Mus musculus

<400> 10

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly
 1 5 10 15

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn

65		70		75		80									
Glu	Lys	Phe	Arg	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser
				85				90					95		
Thr	Ala	Tyr	Ile	Leu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Met
			100					105					110		
Tyr	Phe	Cys	Val	Arg	Ser	Asp	Asp	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
		115					120					125			
Thr	Leu	Thr	Val	Ser	Ser										
	130														

<210> 11
 <211> 384
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1).. (384)
 <223>

<400> 11
 atg cat ttt caa gtg cag att ttc agc ttc ctg cta atc agt gcc tca 48
 Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

 gtc atc atg tcc aga gga caa att gtt ctc acc cag tcg cca gca atc 96
 Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
 20 25 30

 atg tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc 144
 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser

35	40	45
Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe		
50	55	60
Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro		
65	70	75
Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile		
85	90	95
Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg		
100	105	110
Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys		
115	120	125

<210> 13
 <211> 792
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1).. (792)
 <223>

<400> 13	
atg cga tgg agc tgg atc ttt ctc ttc ctc ctg tca ata act gca ggt	48
Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly	
1 5 10 15	
gtc cat tgc cag gtc cag ttg cag cag tct gga cct gag ctg gtg aag	96
Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys	
20 25 30	

cct ggg gct tca gtg aag atg tct tgt aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
aca gac tac ttt ata cac tgg gtg aaa cag agg cct gga cag gga ctt.	192
Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu	
50 55 60	
gaa tgg att gga tgg att ttt cct gga gat gat act act gat tac aat	240
Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn	
65 70 75 80	
gag aag ttc agg ggc aag acc aca ctg act gca gac aaa tcc tcc agc	288
Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser	
85 90 95	
aca gcc tac att ttg ctc agc agc ctg acc tct gag gac tct gcg atg	336
Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met	
100 105 110	
tat ttc tgt gta agg agt gac gac ttt gac tac tgg ggc cag ggc acc	384
Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr	
115 120 125	
act ctc aca gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct	432
Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser	
130 135 140	
ggc ggt ggc gga agc caa att gtt ctc acc cag tcg cca gca atc atg	480
Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met	
145 150 155 160	
tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca	528
Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser	
165 170 175	

agt gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt ccc 576
 Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro
 180 185 190

aaa ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct act 624
 Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr
 195 200 205

cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc agc 672
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
 210 215 220

cga atg gag gct gaa gat gct gcc act tat tac tgc cag caa agg acg 720
 Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr
 225 230 235 240

agt tat cca ccc acg ttc ggc tgc ggg aca aag ttg gag ata aaa gac 768
 Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp
 245 250 255

tac aag gat gac gac gat aag tga 792
 Tyr Lys Asp Asp Asp Asp Lys
 260

<210> 14

<211> 263

<212> PRT

<213> Mus musculus

<400> 14

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly
 1 5 10 15

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn
 65 70 75 80

Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met
 100 105 110

Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
 115 120 125

Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 130 135 140

Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met
 145 150 155 160

Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser
 165 170 175

Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro
 180 185 190

Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr
 195 200 205

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
 210 215 220

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr
 225 230 235 240

Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp
 245 250 255

Tyr Lys Asp Asp Asp Asp Lys
 260

<210> 15

<211> 35

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 15

Cctgaattcc accatgcat ggagctggat ctttc

35

<210> 16

<211> 48

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 16

accgccagag ccacctccgc ctgaaccgcc tccacctgag gagactgt

48

<210> 17

<211> 57
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 17
 ttcaggcgga ggtggctctg gcggtggcgg aagccaaatt gttctcaccc agtcgcc 57

<210> 18
 <211> 63
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 18
 accgatccg ccgccaccac tgccaccacc tccttttatt tccaactttg tccccgagcc 60

gaa 63

<210> 19
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 19
 ggcgatccg gtggcggtgg ctcacaggtc cagttgcagc agtctggacc 50

<210> 20

<211> 68

<212> DNA

<213> Artificial

<220> |

<223> an artificially synthesized primer sequence

<400> 20

attgcggccg cttatcactt atcgtcgtca tccttgtagt cttttatctc caactttgtc 60

cccgagcc 68